Report

	assembly
# contigs (>= 1000 bp)	1
# contigs (>= 5000 bp)	1
# contigs (>= 10000 bp)	1
# contigs (>= 25000 bp)	1
# contigs (>= 50000 bp)	1
Total length (>= 1000 bp)	6789858
Total length (>= 5000 bp)	6789858
Total length (>= 10000 bp)	6789858
Total length (>= 25000 bp)	6789858
Total length (>= 50000 bp)	6789858
# contigs	1
Largest contig	6789858
Total length	6789858
Reference length	6792330
GC (%)	66.17
Reference GC (%)	66.17
N50	6789858
NG50	6789858
N75	6789858
NG75	6789858
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	0
# misassembled contigs	0
Misassembled contigs length	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# unaligned contigs	0 + 0 part
Unaligned length	0
Genome fraction (%)	99.998
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	10.54
# indels per 100 kbp	33.42
Largest alignment	6789858
Total aligned length	6789858
NA50	6789858
NGA50	6789858
NA75	6789858
NGA75	6789858
LA50	1
LGA50	1
LA75	1
LGA75	1

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

Misassemblies report

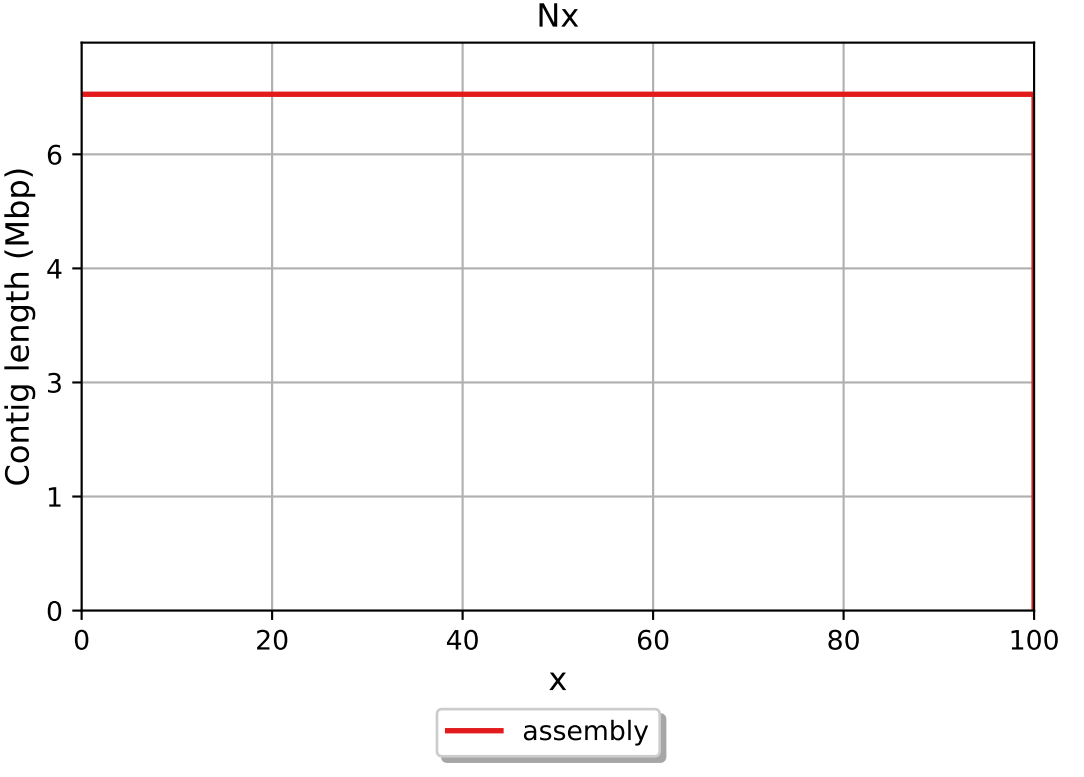
	assembly
# misassemblies	0
# contig misassemblies	0
# c. relocations	0
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	0
Misassembled contigs length	0
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	0
# mismatches	716
# indels	2270
# indels (<= 5 bp)	2266
# indels (> 5 bp)	4
Indels length	2480

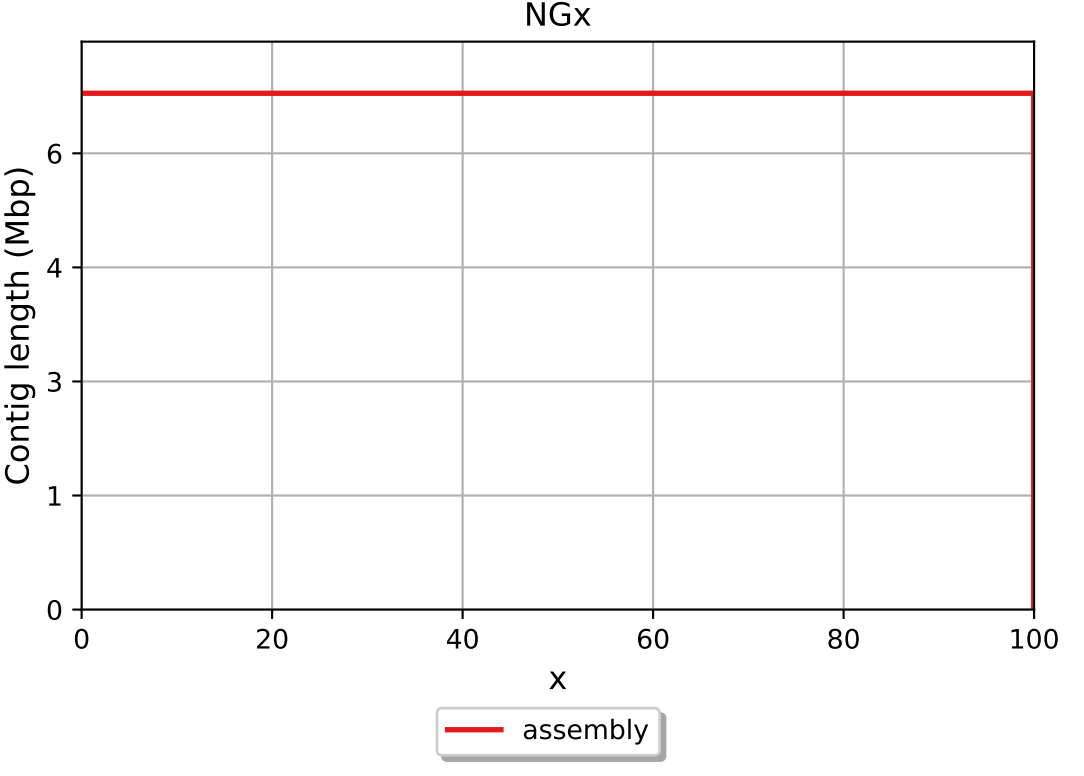
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

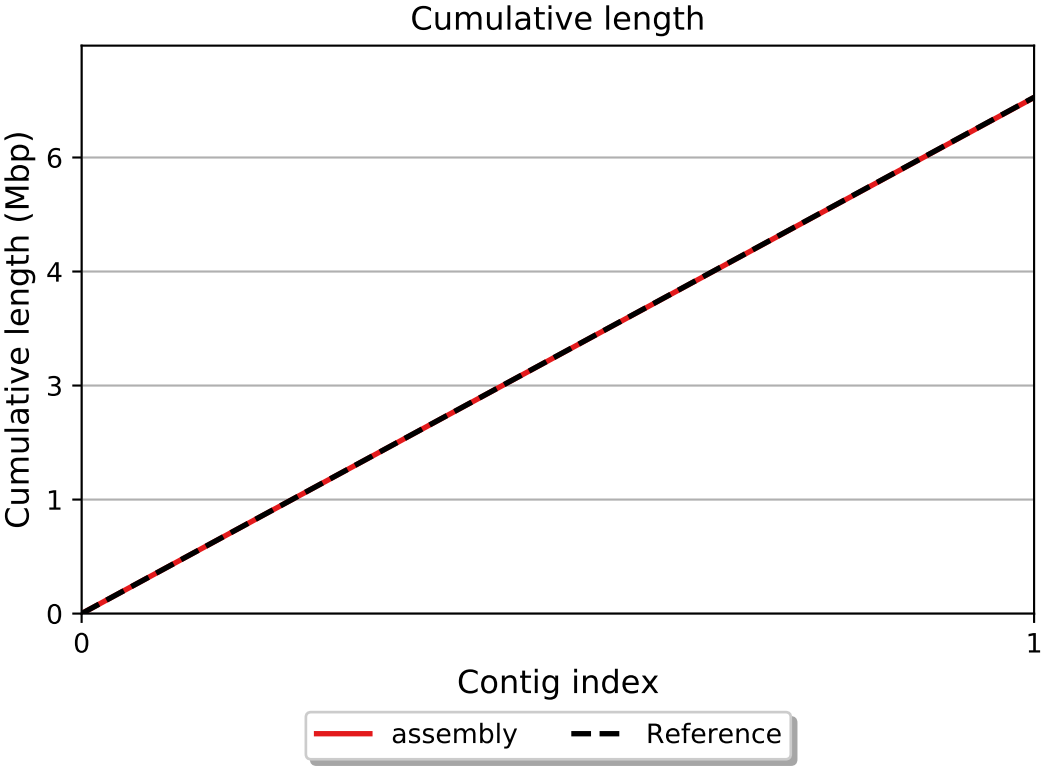
Unaligned report

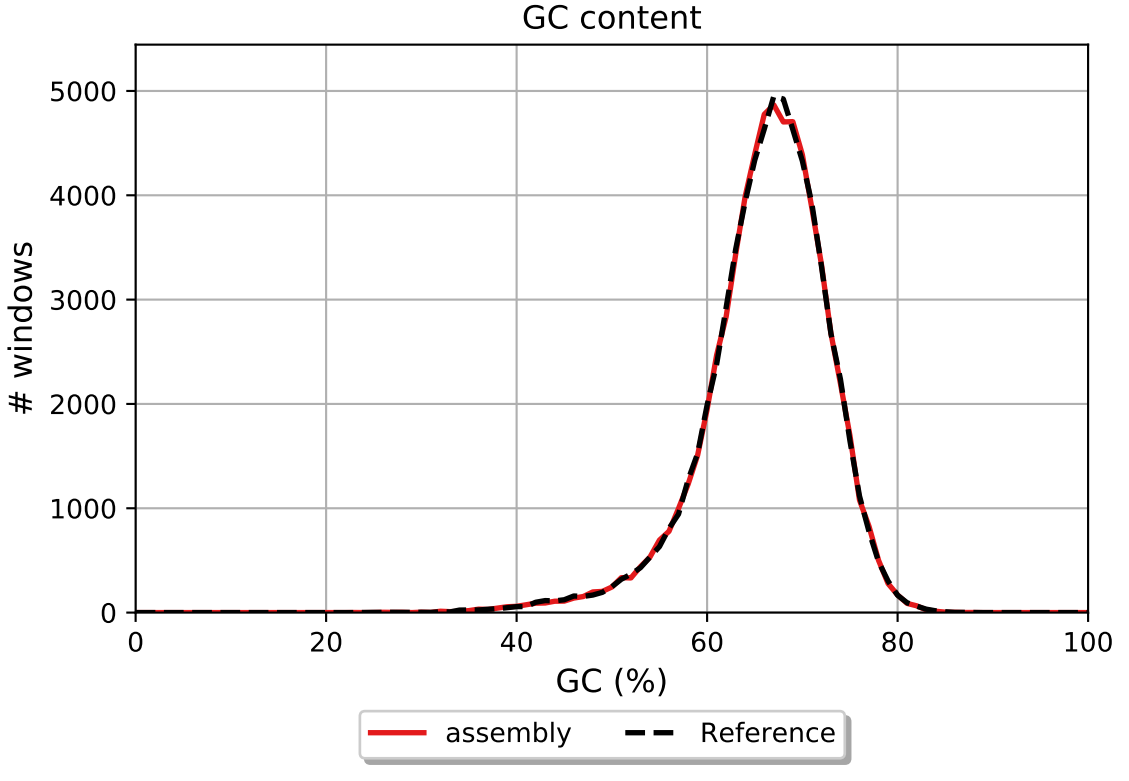
	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	0
Partially unaligned length	0
# N's	0

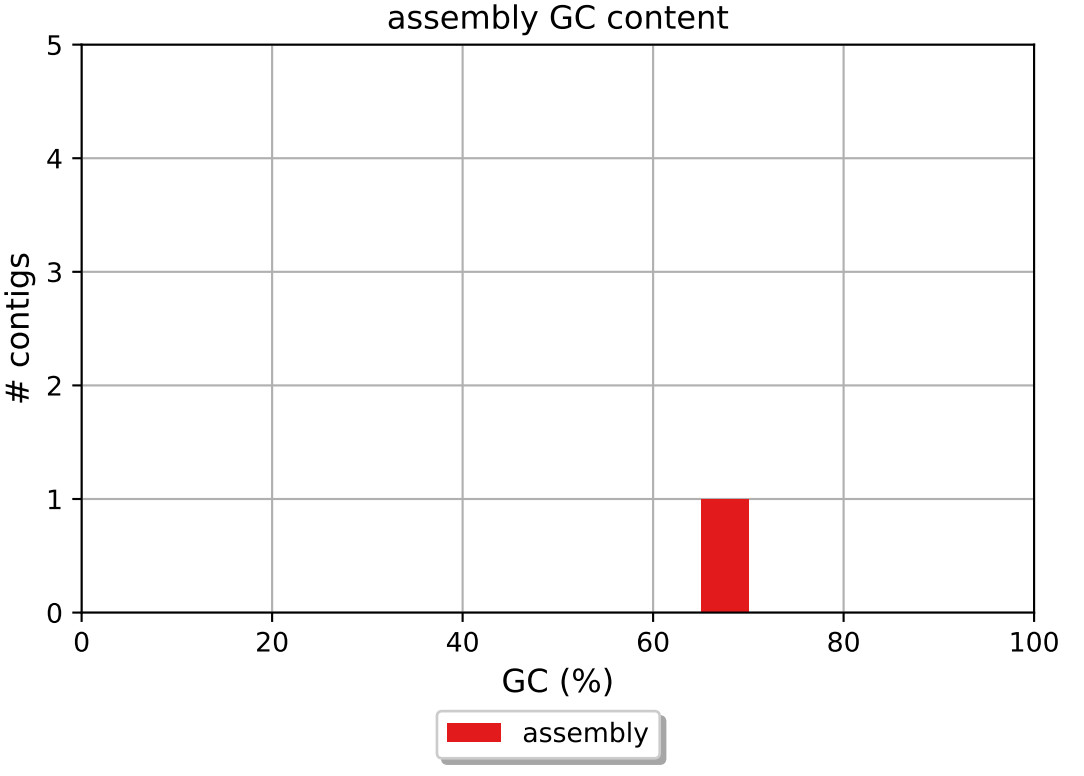
All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

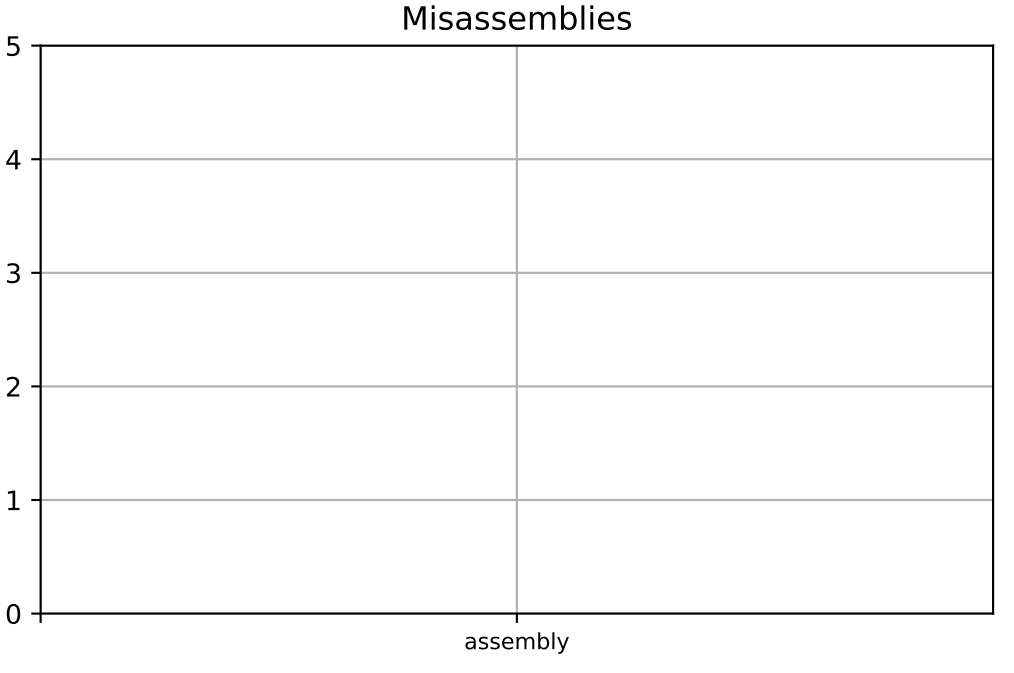

Nx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
assembly

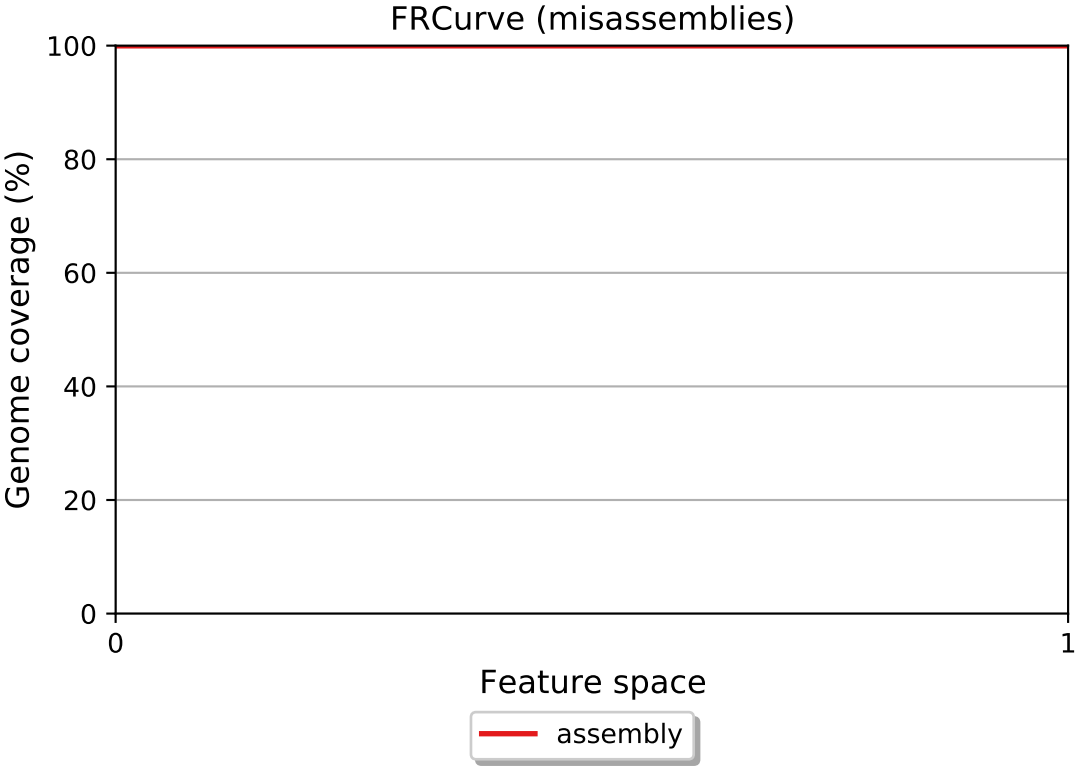

NGx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
assembly

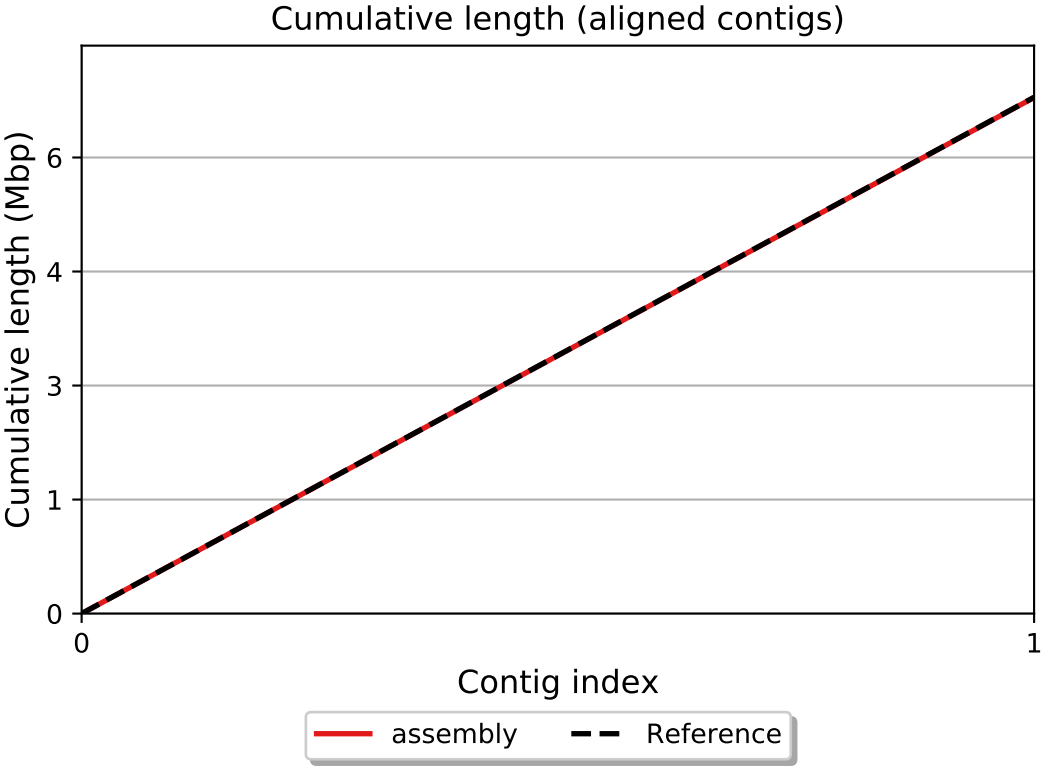

Cumulative length
Cumulative length (Mbp)
0
1
3
4
6
0
1
Contig index
assembly
Reference

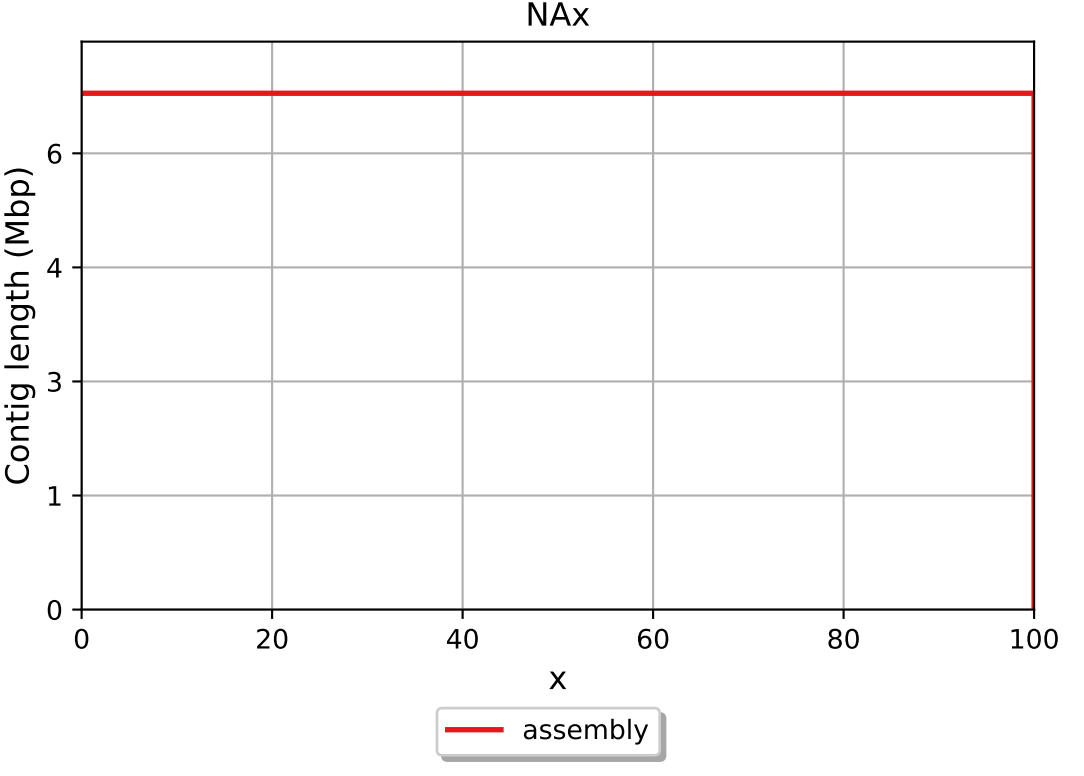

GC content
windows
5000
4000
3000
2000
1000
0
0
20
40
60
80
100
GC (%)
assembly
Reference

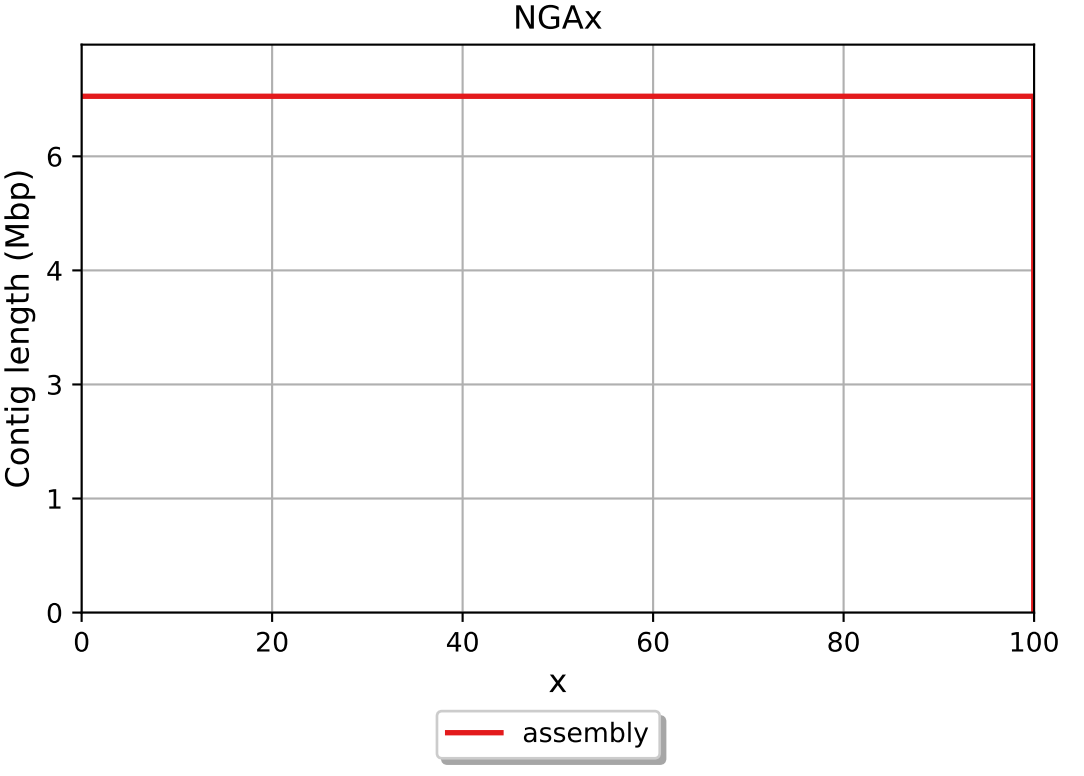

assembly GC content
contigs
GC (%)
0
1
2
3
4
5
0
20
40
60
80
100
assembly


Misassemblies
5
4
3
2
1
0
assembly


FRCurve (misassemblies)
Genome coverage (%)
100
80
60
40
20
0
0
1
Feature space
assembly


Cumulative length (aligned contigs)
Cumulative length (Mbp)
0
1
3
4
6
0
1
Contig index
assembly
Reference


NAx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
assembly


NGAx
Contig length (Mbp)
0
1
3
4
6
0
20
40
60
80
100
x
assembly